

Maite Muniesa

List of Publications by Year in descending order

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92
papers

5,362
citations

61984

43
h-index

88630

70
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92
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92
docs citations

92
times ranked

4943
citing authors

#	ARTICLE	IF	CITATIONS
1	Modeling human pollution in water bodies using somatic coliphages and bacteriophages that infect <i>Bacteroides thetaiotaomicron</i> strain GA17. <i>Journal of Environmental Management</i> , 2022, 301, 113802.	7.8	1
2	Bacteriophages in sewage: abundance, roles, and applications. <i>FEMS Microbes</i> , 2022, 3, .	2.1	15
3	Essential Topics for the Regulatory Consideration of Phages as Clinically Valuable Therapeutic Agents: A Perspective from Spain. <i>Microorganisms</i> , 2022, 10, 717.	3.6	12
4	Antibiotic resistance in the viral fraction of dairy products and a nut-based milk. <i>International Journal of Food Microbiology</i> , 2022, 367, 109590.	4.7	7
5	Chicken liver is a potential reservoir of bacteriophages and phage-derived particles containing antibiotic resistance genes. <i>Microbial Biotechnology</i> , 2022, 15, 2464-2475.	4.2	4
6	Prevalence of bacterial genes in the phage fraction of food viromes. <i>Food Research International</i> , 2022, 156, 111342.	6.2	2
7	Isolation and Characterization of Shiga Toxin Bacteriophages. <i>Methods in Molecular Biology</i> , 2021, 2291, 119-144.	0.9	2
8	Bacteriophages of Shiga Toxin-Producing <i>Escherichia coli</i> and Their Contribution to Pathogenicity. <i>Pathogens</i> , 2021, 10, 404.	2.8	44
9	Bacteriophages as Fecal Pollution Indicators. <i>Viruses</i> , 2021, 13, 1089.	3.3	21
10	Extensive antimicrobial resistance mobilization via multicopy plasmid encapsidation mediated by temperate phages. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 3173-3180.	3.0	25
11	Investigation on the Evolution of Shiga Toxin-Converting Phages Based on Whole Genome Sequencing. <i>Frontiers in Microbiology</i> , 2020, 11, 1472.	3.5	13
12	Antibiotic Resistance Genes in Phage Particles from Antarctic and Mediterranean Seawater Ecosystems. <i>Microorganisms</i> , 2020, 8, 1293.	3.6	33
13	Are Phages Parasites or Symbionts of Bacteria?. , 2020, , 143-162.		2
14	Unravelling the consequences of the bacteriophages in human samples. <i>Scientific Reports</i> , 2020, 10, 6737.	3.3	24
15	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	13.3	184
16	Infectious phage particles packaging antibiotic resistance genes found in meat products and chicken feces. <i>Scientific Reports</i> , 2019, 9, 13281.	3.3	67
17	Faecal phageome of healthy individuals: presence of antibiotic resistance genes and variations caused by ciprofloxacin treatment. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 854-864.	3.0	24
18	Phage particles harboring antibiotic resistance genes in fresh-cut vegetables and agricultural soil. <i>Environment International</i> , 2018, 115, 133-141.	10.0	84

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19	Antibiotic resistance genes in phage particles isolated from human faeces and induced from clinical bacterial isolates. <i>International Journal of Antimicrobial Agents</i> , 2018, 51, 434-442.	2.5	46
20	Isolation of Bacteriophages of the Anaerobic Bacteria <i>Bacteroides</i> . <i>Methods in Molecular Biology</i> , 2018, 1693, 11-22.	0.9	4
21	Detection of Bacteriophage Particles Containing Antibiotic Resistance Genes in the Sputum of Cystic Fibrosis Patients. <i>Frontiers in Microbiology</i> , 2018, 9, 856.	3.5	40
22	The occurrence of antibiotic resistance genes in a Mediterranean river and their persistence in the riverbed sediment. <i>Environmental Pollution</i> , 2017, 223, 384-394.	7.5	106
23	Determination of crAssphage in water samples and applicability for tracking human faecal pollution. <i>Microbial Biotechnology</i> , 2017, 10, 1775-1780.	4.2	96
24	Contribution of cropland to the spread of Shiga toxin phages and the emergence of new Shiga toxin-producing strains. <i>Scientific Reports</i> , 2017, 7, 7796.	3.3	12
25	Is Genetic Mobilization Considered When Using Bacteriophages in Antimicrobial Therapy?. <i>Antibiotics</i> , 2017, 6, 32.	3.7	12
26	Phages in the Human Body. <i>Frontiers in Microbiology</i> , 2017, 8, 566.	3.5	86
27	Coliphages as Model Organisms in the Characterization and Management of Water Resources. <i>Water (Switzerland)</i> , 2016, 8, 199.	2.7	76
28	Heterogeneity in phage induction enables the survival of the lysogenic population. <i>Environmental Microbiology</i> , 2016, 18, 957-969.	3.8	28
29	Bacteriophages in clinical samples can interfere with microbiological diagnostic tools. <i>Scientific Reports</i> , 2016, 6, 33000.	3.3	86
30	Development of new host-specific <i>Bacteroides</i> qPCR's for the identification of fecal contamination sources in water. <i>MicrobiologyOpen</i> , 2016, 5, 83-94.	3.0	30
31	Spread of bacterial genomes in packaged particles. <i>Future Microbiology</i> , 2016, 11, 171-173.	2.0	10
32	Persistence of naturally occurring antibiotic resistance genes in the bacteria and bacteriophage fractions of wastewater. <i>Water Research</i> , 2016, 95, 11-18.	11.3	129
33	Free Shiga toxin encoding bacteriophages are less prevalent than Shiga toxin 2 phages in extraintestinal environments. <i>Environmental Microbiology</i> , 2015, 17, 4790-4801.	3.8	22
34	BaeSR, Involved in Envelope Stress Response, Protects against Lysogenic Conversion by Shiga Toxin 2-Encoding Phages. <i>Infection and Immunity</i> , 2015, 83, 1451-1457.	2.2	4
35	Predicting fecal sources in waters with diverse pollution loads using general and molecular host-specific indicators and applying machine learning methods. <i>Journal of Environmental Management</i> , 2015, 151, 317-325.	7.8	28
36	Transfer of antibiotic-resistance genes via phage-related mobile elements. <i>Plasmid</i> , 2015, 79, 1-7.	1.4	200

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37	Improving Detection of Shiga Toxin-Producing <i>Escherichia coli</i> by Molecular Methods by Reducing the Interference of Free Shiga Toxin-Encoding Bacteriophages. <i>Applied and Environmental Microbiology</i> , 2015, 81, 415-421.	3.1	29
38	Implications of free Shiga toxin-converting bacteriophages occurring outside bacteria for the evolution and the detection of Shiga toxin-producing <i>Escherichia coli</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2014, 4, 46.	3.9	46
39	Antibiotic Resistance Genes in the Bacteriophage DNA Fraction of Human Fecal Samples. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 606-609.	3.2	105
40	Persistence of Infectious Shiga Toxin-Encoding Bacteriophages after Disinfection Treatments. <i>Applied and Environmental Microbiology</i> , 2014, 80, 2142-2149.	3.1	27
41	Bacteriophages infecting <i>Bacteroides</i> as a marker for microbial source tracking. <i>Water Research</i> , 2014, 55, 1-11.	11.3	47
42	Identifying and analyzing bacteriophages in human fecal samples: what could we discover?. <i>Future Microbiology</i> , 2014, 9, 879-886.	2.0	7
43	Antibiotic resistance genes in bacterial and bacteriophage fractions of Tunisian and Spanish wastewaters as markers to compare the antibiotic resistance patterns in each population. <i>Environment International</i> , 2014, 73, 167-175.	10.0	76
44	Quinolone resistance genes (<i>qnrA</i> and <i>qnrS</i>) in bacteriophage particles from wastewater samples and the effect of inducing agents on packaged antibiotic resistance genes. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 1265-1274.	3.0	92
45	Sludge As a Potential Important Source of Antibiotic Resistance Genes in Both the Bacterial and Bacteriophage Fractions. <i>Environmental Science & Technology</i> , 2014, 48, 7602-7611.	10.0	147
46	Potential impact of environmental bacteriophages in spreading antibiotic resistance genes. <i>Future Microbiology</i> , 2013, 8, 739-751.	2.0	91
47	Detection of quinolone-resistant <i>Escherichia coli</i> isolates belonging to clonal groups O25b:H4-B2-ST131 and O25b:H4-D-ST69 in raw sewage and river water in Barcelona, Spain. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 758-765.	3.0	44
48	Shiga Toxin 2-Encoding Bacteriophages in Human Fecal Samples from Healthy Individuals. <i>Applied and Environmental Microbiology</i> , 2013, 79, 4862-4868.	3.1	50
49	Could bacteriophages transfer antibiotic resistance genes from environmental bacteria to human-body associated bacterial populations?. <i>Mobile Genetic Elements</i> , 2013, 3, e25847.	1.8	67
50	Bacteriophage-driven emergence of novel pathogens. <i>Future Virology</i> , 2013, 8, 323-325.	1.8	3
51	Stability and Infectivity of Cytolethal Distending Toxin Type V Gene-Carrying Bacteriophages in a Water Mesocosm and under Different Inactivation Conditions. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5818-5823.	3.1	18
52	Use of abundance ratios of somatic coliphages and bacteriophages of <i>Bacteroides thetaiotaomicron</i> GA17 for microbial source identification. <i>Water Research</i> , 2012, 46, 6410-6418.	11.3	44
53	New Molecular Quantitative PCR Assay for Detection of Host-Specific Bifidobacteriaceae Suitable for Microbial Source Tracking. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5788-5795.	3.1	35
54	Characterizing RecA-Independent Induction of Shiga toxin2-Encoding Phages by EDTA Treatment. <i>PLoS ONE</i> , 2012, 7, e32393.	2.5	87

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55	Shiga Toxin-Producing <i>Escherichia coli</i> O104:H4: a New Challenge for Microbiology. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4065-4073.	3.1	169
56	Type III effector genes and other virulence factors of Shiga toxin-encoding <i>Escherichia coli</i> isolated from wastewater. <i>Environmental Microbiology Reports</i> , 2012, 4, 147-155.	2.4	12
57	Antibiotic Resistance Genes in the Bacteriophage DNA Fraction of Environmental Samples. <i>PLoS ONE</i> , 2011, 6, e17549.	2.5	275
58	Isolation of bacteriophage host strains of <i>Bacteroides</i> species suitable for tracking sources of animal faecal pollution in water. <i>Environmental Microbiology</i> , 2011, 13, 1622-1631.	3.8	32
59	Bacteriophages and genetic mobilization in sewage and faecally polluted environments. <i>Microbial Biotechnology</i> , 2011, 4, 725-734.	4.2	40
60	Quantification and Evaluation of Infectivity of Shiga Toxin-Encoding Bacteriophages in Beef and Salad. <i>Applied and Environmental Microbiology</i> , 2011, 77, 3536-3540.	3.1	28
61	Bacteriophages Carrying Antibiotic Resistance Genes in Fecal Waste from Cattle, Pigs, and Poultry. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 4908-4911.	3.2	136
62	Bacteriophage-Encoding Cytolethal Distending Toxin Type V Gene Induced from Nonclinical <i>Escherichia coli</i> Isolates. <i>Infection and Immunity</i> , 2011, 79, 3262-3272.	2.2	29
63	Quantification of Shiga Toxin-Converting Bacteriophages in Wastewater and in Fecal Samples by Real-Time Quantitative PCR. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5693-5701.	3.1	58
64	Phage-Mediated Shiga Toxin 2 Gene Transfer in Food and Water. <i>Applied and Environmental Microbiology</i> , 2009, 75, 1764-1768.	3.1	55
65	Genotypic and Phenotypic Diversity among Induced, <i>stx2</i> -Carrying Bacteriophages from Environmental <i>Escherichia coli</i> Strains. <i>Applied and Environmental Microbiology</i> , 2009, 75, 329-336.	3.1	52
66	Differential persistence of F-specific RNA phage subgroups hinders their use as single tracers for faecal source tracking in surface water. <i>Water Research</i> , 2009, 43, 1559-1564.	11.3	41
67	Conserved <i>Stx2</i> Phages from <i>Escherichia coli</i> O103:H25 Isolated from Patients Suffering from Hemolytic Uremic Syndrome. <i>Foodborne Pathogens and Disease</i> , 2008, 5, 801-810.	1.8	16
68	Insertion Site Occupancy by <i>stx2</i> Bacteriophages Depends on the Locus Availability of the Host Strain Chromosome. <i>Journal of Bacteriology</i> , 2007, 189, 6645-6654.	2.2	80
69	The application of a recently isolated strain of <i>Bacteroides</i> (GB-124) to identify human sources of faecal pollution in a temperate river catchment. <i>Water Research</i> , 2007, 41, 3683-3690.	11.3	76
70	The contribution of induction of temperate phages to the numbers of free somatic coliphages in waters is not significant. <i>FEMS Microbiology Letters</i> , 2007, 270, 272-276.	1.8	11
71	Occurrence of <i>Escherichia coli</i> O157:H7 and Other Enterohemorrhagic <i>Escherichia coli</i> in the Environment. <i>Environmental Science & Technology</i> , 2006, 40, 7141-7149.	10.0	108
72	Use of the lambda Red recombinase system to produce recombinant prophages carrying antibiotic resistance genes. <i>BMC Molecular Biology</i> , 2006, 7, 31.	3.0	69

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73	Newly identified bacteriophages carrying the stx2g Shiga toxin gene isolated from Escherichia coli strains in polluted waters. FEMS Microbiology Letters, 2006, 258, 127-135.	1.8	30
74	Extended-spectrum β -lactamase-producing Enterobacteriaceae in different environments (humans, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.0	199
75	Active Genetic Elements Present in the Locus of Enterocyte Effacement in Escherichia coli O26 and Their Role in Mobility. Infection and Immunity, 2006, 74, 4190-4199.	2.2	10
76	Integrated Analysis of Established and Novel Microbial and Chemical Methods for Microbial Source Tracking. Applied and Environmental Microbiology, 2006, 72, 5915-5926.	3.1	145
77	Method for Isolation of Bacteroides Bacteriophage Host Strains Suitable for Tracking Sources of Fecal Pollution in Water. Applied and Environmental Microbiology, 2005, 71, 5659-5662.	3.1	83
78	Bacteriophages May Bias Outcome of Bacterial Enrichment Cultures. Applied and Environmental Microbiology, 2005, 71, 4269-4275.	3.1	41
79	Abundance in Sewage of Bacteriophages Infecting <i>Escherichia coli</i> O157:H7. , 2004, 268, 079-088.		20
80	Tracking the origin of faecal pollution in surface water: an ongoing project within the European Union research programme. Journal of Water and Health, 2004, 2, 249-260.	2.6	42
81	Bacteriophages and Diffusion of β -lactamase Genes. Emerging Infectious Diseases, 2004, 10, 1134-1137.	4.3	83
82	Diversity of stx 2 converting bacteriophages induced from Shiga-toxin-producing Escherichia coli strains isolated from cattle. Microbiology (United Kingdom), 2004, 150, 2959-2971.	1.8	135
83	Prevalence of the stx2 Gene in Coliform Populations from Aquatic Environments. Applied and Environmental Microbiology, 2004, 70, 3535-3540.	3.1	43
84	Tracking the origin of faecal pollution in surface water: an ongoing project within the European Union research programme. Journal of Water and Health, 2004, 2, 249-60.	2.6	12
85	Bacterial host strains that support replication of somatic coliphages. Antonie Van Leeuwenhoek, 2003, 83, 305-315.	1.7	37
86	Shiga Toxin 2-Converting Bacteriophages Associated with Clonal Variability in Escherichia coli O157:H7 Strains of Human Origin Isolated from a Single Outbreak. Infection and Immunity, 2003, 71, 4554-4562.	2.2	100
87	Survival of Bacterial Indicator Species and Bacteriophages after Thermal Treatment of Sludge and Sewage. Applied and Environmental Microbiology, 2003, 69, 1452-1456.	3.1	138
88	Optimisation and standardisation of a method for detecting and enumerating bacteriophages infecting Bacteroides fragilis. Journal of Virological Methods, 2001, 93, 127-136.	2.1	28
89	Occurrence of phages infecting Escherichia coli O157:H7 carrying the Stx 2 gene in sewage from different countries. FEMS Microbiology Letters, 2000, 183, 197-200.	1.8	45
90	Characterization of a Shiga Toxin 2e-Converting Bacteriophage from an Escherichia coli Strain of Human Origin. Infection and Immunity, 2000, 68, 4850-4855.	2.2	100

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91	Comparative Survival of Free Shiga Toxin 2-Encoding Phages and <i>Escherichia coli</i> Strains outside the Gut. <i>Applied and Environmental Microbiology</i> , 1999, 65, 5615-5618.	3.1	81
92	Abundance in Sewage of Bacteriophages That Infect <i>Escherichia coli</i> O157:H7 and That Carry the Shiga Toxin 2 Gene. <i>Applied and Environmental Microbiology</i> , 1998, 64, 2443-2448.	3.1	109